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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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CYSE_SALTY
CYSE_HAEIN
CYSE_BUCA1
CYSE_BUCAP
CYSE_SYNP7
CYSE_BACSU
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CYSE_STAXY
NIFP_AZOCH
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SRPH_SYNP7
WCAB_ECOLI
NODL_RHILV
YA64_METJA
THGA_ECOLI
YJV8_YEAST
YA39_SCHPO
                                                                                                                                                                                                                                                                                                                                                                              CYSE_HELPY
                                                                                         LPXA_AQUAE
TABB_PSESZ
CAPG_STAAU
THGA_LACLA
                                                                                                                                                           LPXD_RICRI
                                                                                                                                                                                                             NODL_RHIME
LPXD_RICPR
                       Y304_METJA
WCAF_ECOLI
LPXA_PROMI
LPXA_HAEIN
                                                                                                                                                                                                MAA_BACSU
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            LPXA_YEREN
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p77985 staphylococ
p23145 sacrobacter
p71405 helicobacte
o59967 synechococc
p77558 escherichia
p08632 rhizobium 1
058464 methanococc
p07464 escherichia
p40892 saccharomyc
009707 schizosacch
p28266 rhizobium n
p28266 rhizobium n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p43886 haemophilus
p57162 buchnera ap
p32003 buchnera ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P05796 escherichia
P29847 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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Q56002 synechococc
Q06750 bacillus su
                     p52984 lactococcus
057752 methanococc
p71240 escherichia
p72215 proteus mir
p43887 haemophilus
p32201 yersinia en
                                                                                                        2 aquifex aeo
2 pseudomonas
6 staphylococ
4 lactococcus
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region from Nucleic Acid [4] [4] [4] [4] [4] [6] [6] [6] [7] [6] [7] [6] [7] [7] [7] [7] [7] [7] [7] [7] [7] [7	[2] [2] STRAIN-K12; STRAIN-K92; MEDLINB-902; MEDLINB-902; Tel H., Mura- "Structure avenue in K-12 cy Biochem. Bio [3] STRAIN-K12 / STRAIN-K12 / VANALYSIS H.	scherichia acteria; Pr acherichia; CBI_TaxID=5 CBI_TaxID=5 EQUENCE FRC EQUENCE FRC EDLINE=8800 EDLINE=	OOLI S (SE_ECOLI S 05796; 1988 (Rel 1-NOV-1988 (Rel 1-NOV-1988 (Rel 0-MAY-2000 (Rel 0-MAY-2000 (Rel 0-RINE ACETYLITAL	112.5 6.9 112 6.8 112 6.8 110 6.7 100 6.5 105.5 6.4 104.5 6.3 103.5 6.3 103.5 6.3 103.5 6.3
Res. 22:2576-2586(1994).  Res. 22:2576-2586(1994).  Partick J.P., Shaw W.V.;  Derrick J.P., Shaw W.V.;  Particle and preliminary crystallographic and w.V.;  Moody P.C., Rowe A.J., Shaw	N.A.  (A2; pubMed=2108679;  (K., Kimura A.;  1 expression of cysX, the second gene 3 locus.";  2 locus.";  N.A.  N.A.  N.A.  S00; PubMed=8041620; S00; PubMed=8041620; curland V., Daniels D.L., Plunkett G.  urland V., Daniels D.L., Plunkett G.  curland V., Escherichia coli genome. V. DNA &	pubMed=3309158; pubMed=3309158; thesis in Escherichia coli: nucl thesis eacetyltransferase (cysE) serine acetyltransferase.	ANDARD; PRT; 273 AA.  09, Created) 09, Last sequence update) 09, Last annotation update; NSFERASE (EC 2.3.1.30) (SAT).	456 1 GCAD_BACSU 116 1 GCAD_BACSU 1456 1 GLMU_BCCLI 209 1 SATA_ENTFC 456 1 GLMU_HAEIN 340 1 LPXD_SALTY 341 1 LPXD_HAEIN 171 1 DAPD_BUCAP 275 1 DAPD_BUCAP 275 1 DAPD_BUCAP 275 1 CAT4_BCCLI 210 1 CAT4_BCCLI 210 1 CAT4_MORNO 210 1 CAT4_MORNO ALIGNMENTS
llysis."; ilysis."; is a dimer of COA + O-ACETYL-L-	in the Escherichia	e from the	; ; ;	p14192 bacillus su p42817 bacillus ca p17114 escherichia p50870 enterococcu p43889 haemophilus p18482 salmonella p43888 haemophilus 085290 buchnera ap p45284 haemophilus p23844 agrobacteri p26838 escherichia p50869 morganella

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Submitted (MAY-1991) to the EMBL/GenBank/DDBJ
SEQUENCE FROM N.A. Rogers G.E.;
                                                                                                     Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                    STRAIN-LT2
                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           CYSE_SALTY P29847;
                                                                                                                                                                                                                                                     SALTY
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                                                                                                                                                                                                                                                                                                                            184 GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI 243
                                                                                                                                                                                                                                                                                                                                           223 GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
                                                                                                                                                                                                                                                                                                                   283 IGGKENPRKHDKIPCLTMDQ 302
                                                                                                                                                                                                                                                                                                                                                                              124 GRRALAIFLQNQVSVTFQVDIHÞAAKIGRGIMLDHATGIVVGETAVIENDVSILQSVTLG 183
                                                                                                                                                                                                                                                                                                                                                                                              163 NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 FELFISVLEESPEIIESTKODLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pram; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
SEQUENCE 273 AA; 29316 MW; 466EB898750EF709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A27896; XYECSA.
PIR; A34563; A34563.
ECO2DBASE; H029.3; 6TH EDITION.
ECOGene; EC10187; CYSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EELEIVWNNIKAEARTLADCEPMLASFYHATLLKHENIGSÄLSYMLANKLSSPIMPAIAI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR001451;
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES: COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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50.8%; Pred. No. 3.1e-44;
Mismatches 72; Indels
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                                                                                                                                                                                                                       273 AA.
                                   Rogers G.E.;
                     databases.
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CYSE_HAEIN
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                            SEQUENCE FROM N.A.
STRAIN-ED / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed=7542800;
                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Tocal Similarity
                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                          Haemophilus influenzae.
                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                          P43886;
                                                                                                                                                                                                                                                     CYSE_HAEIN
                                                                                                                                                                                                                                                                                                                      244 VGKPGS----DK-PSMDMDQ 258
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                                                                                                                                                                                                                                                                                                                                                                                                                       124 GRRALAIFLQNQVSVSFQVDIHPAAKIGRGIMLDHATGIVVGETAVIEDDVSILQSVTLG 183
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosyuthesis; Repeat.
SEQUENCE 273 AA; 29291 MW; 6A5736E656FBD25B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 REVVEEAYAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 EDDDDVMIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X59594; CAA42163.1; -: EMBL; A00198; CAA00039.1; -:
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-!- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
-!- PATHWAY: CYSTEINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOHEXAMER. DIMER OF A HOMOTRIHER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACCETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 EELETVWKNIKAEARALADCEPMLASFYHATLLKHENIGSÄLSYMLANKLASPIMPAIAI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cysteine biosypthesis in transgenic animals.";
Patent number GB2227243, 25-JUL-1990.
-!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINF = COA + O-ACETYL-L-
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51.2%; Pred. No. 3.J
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                                                                                                                                                                                                                                             PRT;
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thes 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the swiss Institute of High formatics and the EMBL outstation the swiss institute of High formatics and the EMBL outstation the swiss in t
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Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

PROSITE; PS00101; HEXAPEP, 2.

PS0010132; hexapep; 2.

PS001013
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                                                                                                                                                                                                                                                                                 CYSE_BUCAI STANDARD;
p57162;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence)
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SIMILARITY: BELONGS TO THE CYSE/LACA/LEXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                       Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                        symbiotic bacterium)
                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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(Rel. 40, Last annotation update)
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48.4%; Pred. No. 2.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 AA.
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Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
Nature 407:81-86(2000).
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SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
PROSITES ACYLTRANSFERASES; 553D252F1048B6B1 CRC64;
PROSITES ACYLTRANSFERASES; 1.
PROSITES
                                                                                                                                                                                                                                                                                                                                                                                                                               p32003;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-JUL-1993 (Rel. 39, Last annotation update,
10-MAY-2000 (Rel. 39, CEC 2.3.1.30) (SAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                 Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
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                                                     SEQUENCE FROM N.A. MEDLINE=93012960; PubMed=1398077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPX1/NODL FAMILY OF
                                                                                                                                    endosymbiont of aphids) containing genes homologous
                                                                                                                                                                  Lai C.-Y., Baumann P.;
"Sequence analysis of a DNA fragment from Buchnera aphidicola (an
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=98794;
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     -!- PATHWAY: CYSTEINE BIOSYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSQNRHPTIRKGVVIGAGAKILGNIEVGSGAKIGAGSIVLKNVPSDVTVVGVPAKIV 245
                                      SERINE.
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                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-96281517; PubMed-8661945;

Anandan S., Nalty M.S., Cogdell D.E., Golden S.S.;

"Identification of two classes of transcriptional regulator genes in the cyanobacterium Synechococcus sp. strain PCC 7942.";

Arch. Microbiol. 166:8-63(1996).

-i - CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
                                               -I- SUBCELULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q56002;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 NTGKNRHPIIRKNVTIGAGAKILGNIEVGOGVKVGAGSIVLKNIPPEVTVVGVPAKIIKK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 LSAYLOSRISTVESVDIHPAASIGSGIMLDHATGIVIGEGVIIENDVSIFHSVTLGGTGS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 VALLIONRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK 226
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Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
SEQUENCE 261 AA; 28914 MW; DC02685464A25944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                            PATHWAY: CYSTEINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
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-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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Last annotation update)
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44.1%; Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
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CYSE_BACSU
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                                                                                                                                                                               Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                       "Clustering and co-transcription of the Bacillus subtilis genes encoding the aminoacyl-trNA synthetases specific for glutamate for cysteine and the first enzyme for cysteine biosynthesis.";

J. Biol. Chem. 269:7473-7482(1994).
                                                                                                                                                                                                                                         MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Gagnon Y.,
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94171772; PubMed=7510287;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL1----GGKENPRKHDKIP 296
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                        SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                 PATHWAY: CYSTEINE BIOSYNTHESIS
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                                                                                                                                                          CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE.
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                   non-profit
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        institutions as long
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48.0%;
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Pred. No. 4.4e-27;
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There are no restrictions on ng as its content is in no
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Best Local
                                                     Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3.109-136(1996).
                                                                                                                                                                                                                            "Sakamoto T., Wada H., Nishida I., Ohta H., Murata N.;
"Sequence analysis of a DNA fragment from Synechocystis PCC6803
containing genes homologous to cysE (serine acetyltransferase) and pgi
(glucose-6-phosphate isomerase).";
Plant Mol. Biol. 29:187-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   P74089; Q55209;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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SubtiList; BG10155; cysE.

InterPro; IPR001451; -

Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP TRANSFERASES; 1.

Transferase; Acyltransferase; Cysteine biosynthesis; Resequence 217 AA; 24143 MW; 14EFA32FA1086D9D CRC64;
                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                           SERINE ACETYLTRANSFERASE CYSE OR SLR1348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSE_SYNY3
                                                                                                                                                                    Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E.,
                                                                                                                                                                                   MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
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  SUBCELLULAR
                                         CATALYTIC ACTIVITY: ACETYL-COA +
                PATHWAY: CYSTEINE
                               SERINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L14580; AAA21797.1; -. D26185; BAA05327.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a license agreement (See http://www.isb-sib.ch/announce/
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              BIOSYNTHESIS
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CYTOPLASMIC (BY
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Pred. No. 1.2e-26;
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                                           L-SERINE =
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                                           O-ACETYL-L
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RESULT 9
CYSE_STAXY
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             CYSE_STAXY P77985;
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat.)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001451; -.
Pfam; PF00132; hexapep; 3.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                   FEMS
                                                                                                                                                                  xylosus."
                                                                                                                                                                                                Fiegler
                                                                                                                                                                                                             STRAIN=DSM 20267 / C2A;
MEDLINE=97237691; PubMed=9084146;
                                                                                                                                                                                                                                                                                                      Staphylococcus xylosus
Bacteria; Firmicutes; I
                                                                                                                                                                                                                                                                                                                                       CYSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D13777; BAA02919.1; -. EMBL; D90912; BAA18167.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the EMPL parallel of the surpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                         -!- PATHWAY: CYSTEINE BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC
-!- SIMILARITY: BELONGS TO THE CYSE/Li
                                                                                                                                                                                  "Identification of the
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed.
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                                                       SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-x(4).
                                                                                                                                  CATALYTIC ACTIVITY:
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European
                                                                                                                        SERINE
                                                                                                                                                  Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKIP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFFTGIEIHPGAQIGQGVFIDHGMGVVIGETAIVGDYSLIYQGVTLGGTGXESGKRHPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                Brueckner R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%;
                                                                                                                                    148:181-187(1997).
Y: ACETYL-COA + L-SERINE
                                                                                                                                                                                                                                                                                      Bacillus/Clostridium grus group; Staphylococcus
                                                                                                                                                                                serine acetyltransferase
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Institute.
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Pred. No. 2.
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Best Local
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01-NOV-1991 (Rel. 20, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPKUUL+JI,
Pfam; PF00132; hexapep; 2.
Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
PROSITE: PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
PROSITE: PS00101; PS0010101; PS00101; PS0010101; PS00101; PS00101; PS00101; PS00101; PS001
                                   or send an
                                                                            modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                   Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robson R.L.;

"Nucleotide sequence and genetic analysis of the Azotobacter chroococcum nifusywzm gene cluster, including a new gene (nifp) encodes a serine acetyltransferase.";

J. Bacteriol. 173:5457-5469(1991).

-- FUNCTION: PROBABLE SERINE ACETYLTRANSFERASE REQUIRED FOR OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAY REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR CONCENTRATIONS OF CYSTEINE OR METHIONINE.
EMBL;
                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91358323; PubMed=1885524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZOCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y07614; CAA68887.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Azotobacter
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                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                         SERINE.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                   ACETYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY:
                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIGDNVLIAAGAKVLGNITINANVNIGANSVVLNSVPSYSTVVGIPGHIV--KQDGRRIG
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м60090;
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                                                                                                                                   non-profit institutions as long
                                                      email to license@isb-sib.ch)
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  AAA22162.1;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                               CYSE/LACA/LPXA/NODL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                 MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
                                                                               (See http://www.isb-sib
                                                                                                                                                      There are no restrictions
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                                                                                                     Usage
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                                                                                                                                                                                                                                                                                                                                                   COA + O-ACETYL-L-
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RESULT 11
CYSE_HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                        STRAIN-26695 / AFCC 700392;

STRAIN-26695 / AFCC 700392;

MEDLINE-97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.

Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Sill S., Dougherty

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Sill S., Dougherty

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wal

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSE_HELPY
P71405;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 49503 / 60190;
Peek R.M., Thompson S.A., Atherton J.C., Blass
Peek R.M., Thompson S.A., and the strain of a novel ulcer-associated gene,
Expression of a novel ulcer-associated gene,
following contact with gastric epithelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Nitrogen fixation; Transferase; Acyltransf
Cysteine biosynthesis.
SEQUENCE 269 AA; 28578 MW; EOBBCC982E6
                                                                                                                  pylori.
                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE ACETYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
                                                                                                     Nature 388:539-547(1997)
                                                                                                                                                Venter J.C.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
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                           PATHWAY: CYSTEINE BIOSYNTHESIS
SUBCELLULAR LOCATION: CYTOPLASI
SIMILARITY: BELONGS TO THE CYSI
                                                                       SERINE
                                                                                     CATALYTIC
               ACETYLTRANSFERASES. COMPOSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D43706; D43706. rPro; IPR001451;
                                                                                                                               complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR HP1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLAQWREDIRCVFERDPAARTTFEVLTTYPGVHAIMLYRLAHRLWRPNALPRPAAVVRAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                           (SEP-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori (Campylobacter pylori)
                                                                                      ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
               BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF FERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .. 35, Created)
.. 35, Last sequence upo
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                                                                                     ACETYL-COA +
                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ
                                            CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epsilon
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Helicobacter group;
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             MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                               gastric pathogen Helicobacter
                                                                                      L-SERINE =
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                                                                                      COA +
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                                                                                                                                                                                                                                                     Dougherty
                                                                                        O-ACETYL-L
                                                                                                                                                                                                                                                                                                                                                                                      Miller G.G.;
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                                                                                                                                                                           ley J.M.,
Wallin E
                                                                                                                                                                                                                                                      в.А.,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSE OR JHP1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                             gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
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                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VLQEDPAARNKWEVLLLYPGIHALLCYRLAHALHKRRFYFIARALSQLARFITGIEIHPG 70
                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
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ase; Acyltransferase; Cysteine biosynthesis; Repeat.
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             as its content
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SERINE ACETYLTRANSFERASE, PLASMID (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
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                                                                                                                                                                                                                                                                                                                                       a cyanobacterial plasmid.";
Mol. Gen. Genet. 247:623-632(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPG 186
                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                "Two enzymes together capable of cysteine biosynthesis are encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pANL.
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                   Nicholson M.L., Gaasenbeek M.,
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95327059; PubMed=7603442;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 VLGAICVGDDVRIGANAVVLSDLPTGSTAVGAKAKTI 16
                            PROSITE; PS00101; HEXAPEP_TRANSFERASES;
                                                                               EMBL; U23436; AAA86726.1; -.
                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        -!- PATHWAY: CYSTEINE BIOSYNTHESIS
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   SEQUENCE
               Transferase; Acyltransferase;
                                               Pfam; PF00132; hexapep; 2.
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                                                                InterPro; IPR001451; -.
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                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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     Cysteine biosymhesis;
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RESULT 14
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                                                             MEDLINE-97251358; PubMed-9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
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corresponding to the 40.1-50.0 min region on the linkage map.";
Na Res. 3379-392 (1996).
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                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
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                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                  SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
                                           PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE COLANIC ACID.
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4)
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                                                                                                                                                                                                                                     Canter Cremers H.C.J., Spaink H.P., Wijfjes A.H.M., Pees E., Wijffelman C.A., Okker R.J.H., Lugtenberg B.J.J., "Additional nodulation genes on the Sym plasmid of Rhizobium"
                                                                         Downie J.A.;
                                                                                                                  SIMILARITY TO OTHER MEMBER OF THE CYSE/LACA/NODL FAMILY
                                                                                                                                                                                     leguminosarum biovar viciae.";
Plant Mol. Biol. 13:163-174(1989).
                         "The nodL gene from Rhizobium leguminosarum j
                                                                                                  MEDLINE=90136094; PubMed=2615659
                                                                                                                                                                                                                                                                                                                                        MEDLINE=92003664; PubMed=2562395;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surin B.P., Downie J.A., "Characterization of the Rhizobium leguminosarum genes nodLMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
NODULATION PROTEIN L (EC 2.3.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                           involved in efficient host-specific nodulation. Mol. Microbiol. 2:173-183(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88246045; PubMed=3132583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid sym pRL1JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium leguminosarum (biovar viciae).
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
SEQUENCE 162 AA; 17615 MW; F2462F836F3FB3AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EcoGene; EG13570; wcaB.
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by lacA and cysE. ;;
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RL Mol. Microbiol. 3:1649-1651(1989).

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